REMARKS

Reconsideration is requested.

Claims 1-15 are pending.

Claim 7 has been amended to further specify that the probes of the claimed composition comprise more than 10 contiguous nucleotides. The claims have been amended without prejudice. Support for the amendment to claim 7 can be found, for example, at page 7, lines 14-16. The range of about 10 to about 25 nucleotides described in the specification demonstrates the applicants were in possession of the claimed invention.

Withdrawal of the lack of unity restriction is requested as the claims are patentable over the recited aspect of Fodor (U.S. Patent Application Publication No. 2001/0053519). Specifically, the Examiner is understood to have cited Fodor for the proposition that the alleged teaching in Fodor of a set of every possible 10-mer anticipated claim 7, such that the claims allegedly failed to provide a special technical feature as compared with the art. As claim 7 requires nucleotide sequences of greater than 10-mers however the claims define over the art. The claims share the same or corresponding special technical feature and withdrawal of the lack of unity restriction is requested.

The applicants elect, with traverse, the subject matter of the Examiner's Group I. Withdrawal of the restriction requirement and examination of all of the claims are requested for the reasons noted above.

The further requirement to elect a single allegedly patentable distinct sequence should be withdrawn as the Examiner has failed to establish that the sequences fail to

share the same or corresponding special technical feature. The Examiner's apparent treatment of the sequences according to U.S. restriction practice is submitted, with due respect, to be inappropriate. The present application is a U.S. national phase of a PCT international application such that the principles of unity of invention should be applied for any determination of alleged separate patentability. The Examiner has not demonstrated that the separate sequences lack unity of invention, such as by citation to an anticipatory reference, and as such the requirement to elect a specific sequence should be withdrawn.

Beyond the above, the applicants note that SEQ ID NOs: 1 and 2 are related at least in function and use. Specifically, it has been discovered that the target sequence of the present invention are found in all type of spacer of every Enterococcus species, in particular of every Enterococcus species that are clinically relevant. The target region of target sequence can be defined as a nucleic acid molecule consisting of SEQ ID NO 1 or SEQ ID NO 2, or as a nucleic acid molecule that is homologous to SEQ ID NO 1 or 2, their RNA form wherein T is replaced by U, or their complementary form.

Enterococcus species show a variety of spacer sequences even within one single isolate. Those different ITS vary in length in the range from 200 to 350 base pairs. The variation is mainly caused by the presence or absence of tRNA coding sequences.

To solve the problems generated by this very high variability, the present invention provides a particular region of the ITS, identified and delimited for its great advantage of offering a unique target sequence for the detection and/or identification of *Enterococcus* species , and in particular of *Enterococcus* species clinically relevant,

and more particularly of *Enterococcus faecalis* and *Enterococcus faecium*. It has been discovered that the target sequence of the invention are found in all type of spacer of every *Enterococcus* species, in particular of every *Enterococcus* species that are clinically relevant (see page 6, lines 13-20 of the specification). The target region or target sequence can be defined as a nucleic acid molecule consisting of SEQ ID NO: 1 (derived from *Enterococcus* faecalis) or SEQ ID NO 2 (derived from *Enterococcus* faecium), or as a nucleic acid molecule that is homologous to SEQ ID NOs: 1 or 2, their RNA form wherein T is replaced by U, or their complementary form.

The selection of the sequences SEQ ID NOs: 1 and 2 has been carefully made after comparison of different spacer regions of many Enterococcus species. Based on these sequence data, the unique character of this region was detected, since the region is present in the different spacer regions of the most clinically relevant Enterococcus species and can be amplified with a single primer pair.

The applicants elect, with traverse and for the purposes of being responsive, SEQ ID NO:1. Reconsideration and withdrawal of the requirement for an election of one of SEQ ID NOs: 1 and 2 are requested for at least the reasons noted above.

Clarification of the Examiner's previous comments is noted with appreciation.

The applicants further elect, with traverse, SEQ ID NO:36 of claim 4 in response to the Examiner's further requirement for an election of a sequence of claim 4. Reconsideration and withdrawal of the Examiner's further election requirement are requested as the Examiner has failed to establish that the sequences fail to share the same or corresponding special technical feature. The Examiner's apparent treatment of the sequences according to U.S. restriction practice is submitted, with due respect, to

be inappropriate. The present application is a U.S. national phase of a PCT international application such that the principles of unity of invention should be applied for any determination of alleged separate patentability. The Examiner has not demonstrated that the separate sequences lack unity of invention, such as by citation to an anticipatory reference, and as such the requirement to elect a specific sequence should be withdrawn. Consideration of the following with regard to all of the Examiner's further election requirements is also requested.

The applicants further elect, with traverse, SEQ ID NOs:34 and 69 of claim 6 and 14 in response to the Examiner's further requirement for an election of probes in §(2) on page 3 of the Office Action dated March 22, 2007. Reconsideration and withdrawal of the Examiner's further election requirement are requested as the Examiner has failed to establish that the sequences fail to share the same or corresponding special technical feature. The Examiner's apparent treatment of the sequences according to U.S. restriction practice is submitted, with due respect, to be inappropriate. The present application is a U.S. national phase of a PCT international application such that the principles of unity of invention should be applied for any determination of alleged separate patentability. The Examiner has not demonstrated that the separate sequences lack unity of invention, such as by citation to an anticipatory reference, and as such the requirement to elect a specific sequence should be withdrawn. Consideration of the following with regard to all of the Examiner's further election requirements is also requested.

The applicants further elect, with traverse, SEQ ID NOs:5 and 18 of claim 11 in response to the Examiner's further requirement for an election of primers in §(3) on

page 3 of the Office Action dated March 22, 2007. Reconsideration and withdrawal of the Examiner's further election requirement are requested as the Examiner has failed to establish that the sequences fail to share the same or corresponding special technical feature. The Examiner's apparent treatment of the sequences according to U.S. restriction practice is submitted, with due respect, to be inappropriate. The present application is a U.S. national phase of a PCT international application such that the principles of unity of invention should be applied for any determination of alleged separate patentability. The Examiner has not demonstrated that the separate sequences lack unity of invention, such as by citation to an anticipatory reference, and as such the requirement to elect a specific sequence should be withdrawn. Consideration of the following with regard to all of the Examiner's further election requirements is also requested.

The Examiner is requested to appreciate, with regard to the Examiner's further election requirements in §§(1)-(3) of page 3 of the Office Action dated March 22, 2007, that Table 3, on page 26 of the specification, as well as the accompanying text, teaches sets of two or three probes designed out of the SEQ ID NO: 1 or SEQ ID NO: 2. As is believed to be apparent from the table, each of the sets of probes is able to distinguish between *Enterococcus faecalis/faecium* and *Enterococcus non –faecalis/faecium*. The sets only differ in the degree of legibility of the result (from + to +++).

Evidence that the sets of probes of the claimed invention are able to distinguish between *Enterococcus faecalis/faecium* and *Enterococcus non –faecalis/faecium* is also provided by Example 3, pages 30-31 of the specification, and Example No. 4, page 32 of the specification. Page 32 of the specification summarizes the exemplification as

follows: "All *E. faecalis* and *E. faecium* are detected (Ct & melting curves) and differentiated from other organisms including other *Enterococci*. There are no cross-reactivities observed with other organisms from the many different microorganisms tested, or with human DNA".

The presently claimed invention therefore provide methods and materials to detect *E. faecalis* and/or *E. faecium* as these are the most important species making together up 95% of all nosocomial enterococcal infections. See page 1, lines 21-23, of the specification.

Withdrawal of the further species election requirements is requested.

Rejoinder and allowance of any claim defining a method of making and/or using a product defined by an allowable claim, at an appropriate time, are requested.

An early and favorable Action on the merits of all of the claimed subject matter is requested.

Respectfully submitted,

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